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Title:
Perfect score:
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Listing first 45 summaries
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A Geneseq_23Sep04:*
1: genneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2003s:*
6: geneseqp2003bs:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
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1 QVKLQESGGGLVKPGGSLKL.....TYYCQEWSGYPYTFGGGTKL 237
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

PI Rei	PA (TE	PR 13-	PF 11-	PD 21-	PN-WO2	FT Rec	FT Reg	י אפן אפן	FI		FT Rec	FT Rec	FT Rec	FH Key	OS Mus	KW Major KW viral KW immun XX	DE Mouse	DT 04	AC AAE	AAE38657	DECILIT 1		44 44 45	40 40	38	ນຜູ	ມ ພ 2 ພ ຂ	30 31	28 29	26 27
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  Novel antibody that detecting a cell bea
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Matches 183
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                                                                                                                   Preparation of water-soluble eukaryotic bridges e.g. rPA, comprises cultivation presence of arginine or amide compound.
                                                                                                                                                                                                                 WPI; 2000-674185/66.
N-PSDB; AAC66074.
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Pred. No. 1.2e
24; Mismatches
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                                                                          German.
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                                                                                                                                            polypeptides with disulfide of prokaryotic cells in the
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.2e-62;
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                                                                                                                                                                               Producing naturally folded eukaryotic proteins e.g. interferon, hormones or proteases that contain two of linked by disulfide bridges comprises co-expression
The present invention relates to a method for production of a naturally folded eukaryotic protein containing two or more cysteines linked by disulfide bridges. The method comprises co-expression and secretion into
                                                                                                         Disclosure;
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                                                                                                   Page 19;
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Matches
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This invention describes a novel method for preparing a naturally folded eukaryotic polypeptide (I) that contains two or more disulfide-bridged Cys residues by culturing prokaryotic signal sequence at its N-terminus and a nucleic acid (II) that secretes a chaperone protein (III) into the periplasm. (I) is secreted into the periplasm or medium; the signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the periplasm of a molecular chaperone via an expression vector coding for the chaperone. The expression vector also encodes a signal sequence. The method is useful for producing a naturally folded eukaryotic protein such as an antibody, antibody fragment, interferon, protein hormone or a protease containing two or several cysteines linked by disulfide bridges. The present sequence is a fusion protein composed of the PelB signal sequence and ScFvOxazolon. This sequence was used in the method of the
                                                                                               Disclosure;
                                                                                                                       simultaneous expression o
from periplasm or medium.
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                                                                                                                                                                                                                                                                                                                                                           Synthetic
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DB; AAF61193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY
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                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmid
                                                                                                                                                                                                                                                                                                                                                                                                   protein; periplasm; antibody production;
production; protease production.
                                                                                             Page 20-21; 36pp; German.
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Pred. No. 3e-62;
19; Mismatches
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                                                                                                                                     eukaryotic prote
aperone protein,
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tein, allows simple
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N-PSDB;
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                                                  Example
                                                                                                     expression a specific
                                                                                                                     Producing water-soluble, naturally folded, and secreted eukaryotic polypeptide, involves culturing prokaryotic cells containing an expression vector encoding the polypeptide in the presence of argin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secreted protein; chaperone; interferon; protease; hormone; naturally folded protein; lac promoter; Dnad; heat shock protein; pectate lyase B; PelB; hapten; single-chain Fv-fragment Oxazolon; scFvOxazolon; fusion protein; thyroid stimulating hormone; TSH.
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DB; AAD02212.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARGNWEGWYFDVWGQGTTVTVSSG 120
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Pred. No. 3e-62;
                                               English
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patent discloses a

method for the production of

a water-soluble,

WPI; 1999-611066/52. N-PSDB; AAZ20266.

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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09-APR-1998;
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Pred. No. 3e-62;
9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC The present sequence represents a single chain antibody (scAb) that has 2 CC c-myc epitopes. The scAb is used in claimed methods for localizing a CC probe and for detecting a post-translational activity in a cell, and is CC expressed by a claimed transgenic non-human animal. The invention CC provides methods and reagents for targeting probes to selected cellular CC locations through the expression of specific binding partners (such as CC scAbs) within a cell, and for creating assays for post-translational CC activities. The invention allows the monitoring of the location of such CC intracellular, specific binding partners over time and in response to CC stimuli, such as test chemicals. Spectroscopic probes can be used to CC screen a test chemical for activity. The invention also includes cells and transgenic organisms comprising the intracellular specific binding partner, where the specific binding partner can bind with the cell arms and can be designed to binding partner can bind with the CC cell and can be designed to bind a wide variety of spectroscopic probes, CC including small molecules that have better (and more diverse) spectroscopic properties than green fluorescent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Sim
Matches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Localizing probes to specific sites antibody reactive with probe-ligand post-translational modification and
                                                                                                                         EP1321524-A1
                                                                                                                                                                             Transgenic; biomolecule; ATP; ADP; cytostatic; virucide; gene therapy; antisense therapy; scFv; antibody.
                                                                                                                                                                                                                       Single-chain
                                                                                                                                                                                                                                                                                                       ABR62010 standard; protein;
                                         19-DEC-2001; 2001EP-00130319
                                                                     19-DEC-2001; 2001EP-00130319.
                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                   03-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGSGGGGSGGGSNIELTQSPAIMSASPGERVTMTCSASSSIRYIYWYQQKPGSSPRLL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKKLEWVATISSGGSYTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGSGGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRW 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDSVKGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCARGNWEGWYFDVWGQGTTVTVSSG 120
                                                                                                                                                                                                                                                                                                                                                                            IYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTEGAGTKL
                                                                                                                                                                                                                                                                                                                                                                                               IYDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARD----YGAYWGQGTTVTVSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                       (scfv) antibody
                                                                                                                                                                                                                                                   (first
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                                                                                                                                                                                                                                                 entry)
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78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 976.5;
Pred. No. 4.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.5e-62;
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 17-MAY-2001; 2001WO-DE001916
                            17-JAN-2002
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RESULT 9
AAM48925
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to increasing the content of one or more transgene-coded biomolecules in an organism and involves changing the distribution of ATP and/or ADP in cells of the organism. The yield of transgenic molecules in host cells is often insufficient for industrial production. The method increases the yield of transgenic molecules in animal and plant host cells, therefore facilitating their production on an industrial scale. The proteins produced by the method are useful for diagnosing, preventing and/or treating viral diseases and cancer. The present sequence represents a single-chain (scFv) antibodies in transgenic exemplify the increase in the expression of scFv antibodies in transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Increasing the content of transgene-coded biomolecules in a plant or animal, useful for producing proteins for diagnosing, preventing and/or treating viral diseases and cancer, comprises changing the distribution of ATP and/or ADP.
                                                                                                                                                                                                                           BCFV
                                                                                                                                     Unidentified
                                                                                                                                                                    Ketone binding protein; oxazole; pathogen fungicide; antibacterial; scFv antibody.
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WO200204020-A2
                                                   Misc-difference
                                                                                  Misc-difference
                                                                                                                                                                                                                                                             03-MAY-2002
                                                                                                                                                                                                                                                                                                AAM48925;
                                                                                                                                                                                                                                                                                                                               AAM48925 standard; protein; 241
                                                                                                                                                                                                                         antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           YDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARGNWEGWYFDVWGQGTTVTVSSGG
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                                                                                   Location/Qualifiers
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78.4%;
                                                                 "encoded by CAG"
                               "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
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Pred. No. 2.4e-61;
19; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                          resistance; virucide
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Best Local S
Matches 183
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                                                                                                                                                                                                                                                 Primer; human; immunoglobulin; Ig; variable region; VH; VL; Ck; JH; lymphocyte; vector; soluble; antibody; phage; linker; back; VH3; nested; in-cell PCR; cloning; polymorphic; TCR V; antiphenyloxazolone; hybridoma; NQ2/12.4; NQ10/12.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
19-JUN-1993
                                                                             Peptide
                                                                                                                             Region
                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                    VH NQ10/12.5-Vk NQ10/12.5 linked peptide sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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ide that binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARGNWEGWYFDVWGQGTTVTVSSGG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGSGGGGGGGDIELTGSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARD----YGAYWGQGTTVTVSSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDTSKLSSGVPARFSGSGSGTSVSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                        1. .115
/label= VH_NQ10/12.5
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                                                /note= "Linker peptide"
                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.6%;
77.5%;
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                             . 236
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Vkappa_NQ10/12.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 949.5; DB 5
Pred. No. 2.9e-60;
9; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
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RESULT 11
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Best Local Similarity
Matches 182; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences given in AAR32840-43 show the mature heavy chain VH domains and the VK light chain genes of the antiphenyloxazolone hybridomas NQ2/12.4 and NQ10/12.5 which have been linked via a linker peptide by incell PCR. The cDNA encoding these peptides was synthesised using forward primers annealing to the Ck gene and the JH segment, followed by assembly with linker primers, VH back primers based on the VH3 leader sequence and a forward Ck primer nested in respect to the primer used for cDNA. The assembled product within the cells is then amplified with nested primers annealing to the 5' end of the VH gene and the 3' end of the JK segment. In-cell PCR may be used to determine gene linkage analysis, particularly for the cloning of gene combinations that are polymorphic within a population of cells, such as the rearranged genes for Ig or TCR V regions. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                               AAB20436 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 4; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treatment of cell populations, partic. copies of 2 or more non-contiguous DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-AUG-1991;
11-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                 VKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYYP
                                                                                                                                                                                                                                            YDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL
                                                                                                                                                                                                                                                                         GGSGGGGGGGGGQIVLTQSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWI
                                                                                                                                                                                                                                                                                                                                 DTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARD----YGAYWGQGTLVTVSAGG
                                                                                                                                                                                                                                                                                                                                                                                     VQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYYA
                                                                                                                                                                                                                    YDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKL
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92GB-00012419
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Pred. No. 4e-6'
19; Mismatches
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No. 4e-60;
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sequences t
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facilitate
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176 181

Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; Factor VIII cofactor; blood coagulation disorder; haemorrhagic diathesis; haemostatic; amidolytic; t

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entry)

198/A1

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Best Local
                                                                                                                                                         Matches 178;
                                                                                                                                                                                                                                                The present sequence is that of a single chain Fv (scFv) derivative of antibody 198/A1, comprising the heavy (VH) and light (VL) chain variable regions of 198/A1 joined by an artificial, flexible linker peptide. The scFv was obtained by PCR amplification of cDNAs for 198/A1 VH and VL regions and cloning in vector pDAP2. 198/A1 is an example of anti-human Factor IX (FIX) antibodies of the invention. Anti-FIX/FIXa and their derivatives, including scFv and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor activity or FIXa activating activity. Administration leads to an increase in the procoagulant activity of FIXa, even in the presence of FVIIIa inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIIIa, and in the case of FVIII inhibitor patients. The antibodies and derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
Synthetic.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New factor IX/factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as hemophilia A and hemorrhagic diathesis
                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 10; Fig 17; 138pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scheiflinger F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-1999;
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                                                                                                                                                                      Local Similarity
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SSGGGGSGGGGSNIELTQSPAIMSASPGERVTMTCSASSSI-----RYIYWYQQK
                                                                                                                 QVKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYY
                                                                                                                                                                                                                249
                                                                 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCAR---GNWEGWYFDVWGQGTTVTV
                                                                                                EVQLQESGGGLVKPGGSLKLSCAASGFIFSSYTMSWVRQTPEKKLEWVATISSGGSSTYY
                                          PDSVKGRFTISRDNAKNTLYLOMSSLKSEDTAMYHCTREGGGYYVNWYFDVWGAGTTLTV
                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "encoded by ACN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= CDR3
23. .136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label= VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "encoded by GCN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label= Linker
                                                                                                                                                                    73.6%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .111
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                                                                                                                                                       26;
                                                                                                                                                                      Score 936; DB 4;
Pred. No. 2.8e-59;
                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Falkner F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dorner
                                                                                                                                                                                Length 249
                                                                                                                                                         Indels
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                                                                                                                                                      Gaps
                 172
                                                                      117
                                             120
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CC Genetic selection in microorganisms, for ligand binding proteins (LBP) CC comprises: extracytoplasmic presentation of LBP and; using the signal of CC ligand binding (by signal transduction on the biosynthetic machinery of CC the microorganisms) to express a detectable or selectable function. CC Microorganisms for this process include a genetically stable (CC detection/selection and are transformed with a replicon encoding a fusion protein consisting of the LBP, a transmembrane helix and regulatory CC domain. The detection/selection function is expression of a beta-cc galactosidase gene, integrated into the chromosome and under the control of the ctx (cholera toxin) promoter. The transmembrane helix is taken CC from the toxR gene. Four primers (AAQ8045-56) were used in the CC construction of the plasmid pHKTOXSCFV. The primers described in AAQ8045-60 were used to amplify variable heavy chain sequence of the single CC chain antibody NGIO.1.2.5 and those described in AAQ8045-60 were used to amplified sequences were cloned into the plasmid pHKTOXREI (See CC AAQ8045-56 for details) to create a toxR-seFV fusion gene. This sequence is the single chain antibody (ScFV). (Updated on 25-MAR-2003 to correct pN field.)
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AAR68613
                                                                                             TO COLORO COLORO
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Query Match
Best Local Similarity
                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetic selection of ligand binding proteins in microorganisms - lextracytoplasmic protein presentation, then use of ligand binding express a detectable or selectable function.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetic selection; ligand binding protein; cholera toxin; promoter; detection; selection; beta galactosidase; lac; transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
13-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulatory domain; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BEHW ) BEHRINGWERKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1995-023689/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ80468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hennecke F,
                                                                       ٦<u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 4; 25pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody (scFV) which binds to phenyloxazolone
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No. 2.9e-59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86; T cell activation; inhibitor; graft versus host disease; transplant rejection; altoimmune disease; allergy; transplant rejection; altoimmune disease; allergy; human; bispecific tetravalent antibody; BiTAb;
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                                             (INNO-) INNOGENETICS
                                                                                                                                                                                                                                                                                                                                               Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARD----YGAYWGQGTLVTVSSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGSGGGGGGGGQIVLTQSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARGNWEGWYFDVWGQGTTVTVSSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQLVELGGGFVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKKLEWVATISSGGSYTYYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YDTSKLSSGVPARFSGSGSTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKL
    Sablon
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427. .4
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551. .5
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121. .135
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    Buyse M,
                                                                                                                                                                                                                                                                                   "VL region
                                                                                                                                                                                                                                                                                                                           "(G4S3)flexible linker"
                                                                                                                                                                                                                                                                                                                                                                                                        "human
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "helix-turn-helix dimerisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "human IgG3 hinge region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "VL region anti B7.2 MAb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "(G4S3) flexible linker"
                                                                                                                                                                                                                                             "His6 tag"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This polypeptide comprises the bispecific tetravalent antibody BiTAb1G10-CC B7-24H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2 CC anti B7.2 scFvs (tetravalency). One single BiTAb is a homodimer of 2 CC identical molecules, each containing both an anti B7.1 and anti B7.2 scFv (bispecificity). An anti-B7.1 and and anti-B7.2 scFv are linked using a CC dimerisation domain (see AAW90219), which drives the homodimerisation of CC the molecule. DNA (see AAW90219), which drives the homodimerisation of CC cross-links, and/or cross-reacts, with the costimulatory molecules B7.1 CC and B7.2 that are expressed on the membrane of professional antigen-CC presenting cells, leading to the inhibition of antigen-specific T cell CC activation. The invention relates to such B7-binding molecules, methods CC for their production, and their use for treating or preventing diseases CC of the immune system, in particular graft rejection, graft versus host very
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 178
                                                                                                                                                                                         T cell activation; costimulatory molecule; B7.1; CD80; B7.2; CD86; transplant rejection; allograft rejection; autoimmune disease; therapy; human; bispecific tetravalent antibody; BiTAb; BiTAbB7-24-1G10H6.
                                                                                                  Synthetic. Chimeric.
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                                                                                                                                                                                                                                                                                                                        Bispecific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New molecules which bind B7.1 and B7.2 - useful immune diseases including allograft rejection.
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N-PSDB; AAX01652.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLIYDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGSGGGGSGGGSNIELTQSPAIMSASPGERVTMTCSASSSI--RYIYWYQQXPGSSPR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADSVKGRFTISRDNAKNTLFLQMNSLRAEDTAVYYCAR---DGWYFDVWGQGTTVIVSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARGNWEGWYFDVWGQGTTVTVSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVKLQESGGGLVKPGGSLKLSCAASGFTESSYGMSWVRQTPDKKLEWVATISSGGSYTYY
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                                                                                                                                                                                                                                                                                                                           tetravalent antibody BiTAbB7-24-IG10H6.
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Location/Qualifiers
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                      "pelB signal peptide"
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Pred. No. 1.2e-58;
5; Mismatches 31;
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                                                                                                                                  This polypeptide comprises the bispecific tetravalent antibody BiTAbB7-24 c-1G10H6. The molecule consists of 4 scPvs, i.e. 2 anti B7.1 scFvs and 2 anti B7.2 scFvs (tetravalency). One single BiTAb is a homodimer of 2 identical molecule, each containing both an anti B7.1 and anti B7.2 scFv (bispecificity). An anti-B7.1 and and anti-B7.2 scFv are linked using a chimerisation domain (see AAW90219), which drives the homodimerisation of the molecule. DNA (see AAW90219), which drives the homodimerisation of the molecule. DNA (see AAW90219), which drives the homodimerisation of cross-links, and/or cross-reacts, with the costimulatory molecules B7.1 cand B7.2 that are expressed on the membrane of professional antigen-specific T cell activation. The invention relates to such B7-binding molecules, methods for their production, and their use for treating or preventing diseases of the immune system, in particular graft rejection, graft versus host construction activation altergy and autoimmune diseases (claimed)
                                                                            Query Match
Best Local S
Matches 178
                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                       Example
                                                                                                                                                                                                                                                                                                                                                                                                             New molecules which bind 87.1 and 87.2 - useful to
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-105615/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lorre K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                              lmmune diseases including
 5
                          23
                                                  ш
                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX01651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INNOGENETICS
                                          QVKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYY
                                                                                                                                580
PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARGNWEGWYFDVWGQGTTVTVSSG
                          QVQLQESGGGLVQPGGSRRLSCAASGFTFSSFGMHWVRQAPGKGLEWVAFISSVSTLIYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sablon E,
                                                                              Conservative
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575. .5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "human IgG3 hinge region"
274. .308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "codons for these amino acids are not present in the DNA sequence for BTiTAbB7-24-1G1-H6 provided in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "VH region anti B7.1 MAb"
139. .153
/note= "(G4S3) flexible linker"
154. .262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "VL region anti B7.1 MAb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note=
                                                                                         73.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Виуве М,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "VL region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "VH region anti B7.2 MAb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "human IgG3 hinge domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "helix-turn-helix dimerisation domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "(G4S3)flexible linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "His6 tag'
                                                                                                                                                                                                                                                                                                                                                                                                allograft rejection.
                                                                                                                                                                                                                                                                                                                                                                     English
                                                                           Score 932.5; DB 2
Pred. No. 1.2e-58;
5; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bosman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIG.
                                                                                                    DB 2;
                                                                                                  Length
                                                                            Indels
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RESULT 15
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The invention relates to peptides which are able to confer stability and solubility to an antibody comprising these peptides. The peptides are especially H-FR1, H-FR2, H-FR3 or L-FR4 present within a variable region of an antibody which makes the antibody soluble and stable in cytoplasm. Peptides having the sequences of HFR1 to H-FR4 are present within the variable region of the heavy chain of an antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order (H-FR1)-(H-CDR2)-(H-FR3)-(H-FR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-CDR3)-(H-
                                                                                                                                                                                                                                                                                                                   Peptides which are able to confer stability and solubility to an antibody comprising these peptides, useful for treating pathologies (e.g. tumor) associated with accumulation of a molecule inside or outside a human, or animal cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Protein
                                                                                                                                                                                                                                                                   Example 1; Page 81; 109pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cucumber mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial; antiviral; cytostatic; immunomodulatory; antibody; gene therapy; HIV; light chain; human immunodeficiency virus; tumour metabolic disorder; immune disorder; auto-immune disorder; scFv(P8);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU07497;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Benvenuto E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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DB; AAS11887.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PWIYGTSNLASGVPSRFSGSGSGTDYTLTISSMQPEDAATYYCQQWSSYPLTFGQGTKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGSGGGGGGSDIELTQSPSSMAASVGDRVTITCSVSSRISSSNLHWYQQKSETSPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody scFv(F8).
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/label= Linker_peptide
/note= "This peptide is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .125
/label= VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Heavy chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Light chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 252
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Best Local Similarity 72.6%
Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDR1, L-CDR2, L-CDR3 in the order (L-FR1)-(L-CDR1)-(L-FR2)-(L-FR2)-(L-FR3)-(L-CDR3)-(L-CDR4). The antibodies and polynucleotides (e.g. by gene therapy) are useful for the manufacture of a medicament for the treatment of pathologies associated with accumulation of a molecule inside or outside a human, animal cell or plant cell. The pathologies are infectious (e.g. viral infections such as HIV, human immunodeficiency virus, infections), tumour, metabolic and immune (especially auto-immune) pathologies. The present sequence represents the synthetic antibody scFv(F8) which is used as a basis for constructing synthetic antibodies incorporating the peptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 252 AA;
                                                                     241
                                                                                                      230
                                                                                                                                          181
                                                                                                                                                                           170
                                                                                                                                                                                                              121
                                                                                                                                                                                                                            115 VTVSSGGGGSGGGGSGGGSNIELTQSPAIMSASPGERVTMTCSASSSI-----RYIYWY 169
                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                  61 PDSVKGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCA-RGNWEGW-----YFDVWGQGTT 114
                                                                                                                                                                                                                                                                                                                                                 1 QVQLQESGGDLVQPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLELVATINSNGGSTFY
                                                                                                                                                                                                                                                                                                                                                                     TVSSGGGSGGGGGGGGIELTQSPASLAVSLQRATISCRASESVDSYGNSFWHWY
                                                                     TFGGGTKL 248
                                                                                                      TFGGGTKL 237
                                                                                                                                                                                                                                                                                 PDSVKGRFTISRDNAKNTLYLOMSSLKSEDTAMYYCARRRNYPYYYGSRGYFDYWGQGTT
                                                                                                                                                                                                                                                                                                                                                                                                                     72.8%; Score 926.5; DB 4; Length 252; 72.6%; Pred. No. 1.4e-58; tive 26; Mismatches 31; Indels 11;
              8
              2004, 17:16:45
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Perfect score:
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                                                                                                  single chain Fv antibody - mouse (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995 C;Accession: S41374 R;Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U. submitted to the EMBL Data Library, January 1994 A;Description: Construction and functional characterization of a single chain Fv antibo A;Reference number: S41374 A;Accession: S41374
   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <AR7
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476.5	477	478	479	480.5	480.5	481	482	482.5	482.5	483.5	488.5	491	492.5	493	493
37.5	37.5	37.6	37.7	37.8	37.8	37.8	37.9	37.9	37.9	38.0	38.4	38.6	38.7	38.8	38.8
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137780	PH1007	C34903	D36005	S31669	H27887	A43413	S31666	B27888	PH1010	S12953 ·	S63597	PH0098	A27889	S20641	рн1006
Ig variable region	Ig heavy chain V r	Ig heavy chain pre	Ig heavy chain V r			Ig heavy chain V r							•	Ig heavy chain V r	Ig heavy chain V r

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A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Accession: A56446
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed on M13 is functional: A;Reference number: A56446; MUID:95229583; PMID:7713873
A;Accession: A56446
A;Status: preliminary
A;Cross-references: GB:U20617
C;Keywords: heterotetramer; immunoglobulin
182 VYYTSHLPPGVPARFSGSGSGNSYSLTISSMEGEDAATYYCOOFTSSPFTFGSGTKL
                                                                                                                                          121 GGGSGGGGSGGGSNIELTQSPAIMSASPGERVTMTCSASSSIRYIYMYQQKPGSSPRLL 180
                                                                                                                                                                                                                                                                                                                                                                                            1 QVKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYY
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                                      IYDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL
                                                                                                             GGGSGGGDSGGGGSDIELTQSPAIMSASLGEKVTMSCRASSSVNFIYWYQQKSDASPKLW 181
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C;Species:
C;Date: 15
C;Accessic
R;Jannot,
Ig heavy chain V region pe20 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-OCt-1995 #sequence_revision 03-Nov-1995 #text_change
C;Accession: 855536
C;Accession: 855536
C;Accession: 855536
C;Accession: 85536
C;Accession:
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C;Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change
C;Accession: UC5322
R;Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A;Title: Characterization of scFv-421, a single-chain antibody
A;Reference number: JC5322; MUID:97168950; PMID:9016757
A;Accession: JC5322
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A; Residues: 1-233 <JAN>
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Best Local S
Matches 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPRFQDKATÍTADTSSNTAYLLLSSLTSEDTÁVÝÝCÁRRDTLYTSLGYWGQGSTVTVSSR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSGGGGSGGGSNIELTQSPAIMSASPGERVTMTCSASSSI-----RYIYWYQQKPGSSP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVKA--TMTADTSSNTAYLOLSSLTSEDTAVYYCNAG-----MDYWGOGTTVTVSSGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGSGGGSGGGGSNIELTQSPAIMSASPGERVTMTCSASSSI------RYIYWYQQKPG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYY
                                                                                                                                                                                                                                                                                                                                              RLLIYLVSNLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYCOHIRELTRS-EGGTKL
                                                                                                                                                                                                                                                                                                                                                                                          RLLIYDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSGGRASGGGGSDIELTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWNQQKPGQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARGNWEGWYFDVWGQGTTVTVSSGGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QESGAELVRSGASVKLSCTTSGFNINDYYMHWVKKRPEQGLEWIGRIDPENGDADMTRSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATI--SSGGSYTYYPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 631; DB 2; Length 233; Pred. No. 1e-36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 697; DB 2; Length 249; Pred. No. 3.1e-41;
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   anti-proenkephalin antibodies
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                                                                                                                             23-Jul-1999
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A;Molecule type: DNA
A;Residues: 1-119 <CAT>
A;Residues: 1-119 <CAT>
A;Residues: 1-119 <CAT>
A;Residues: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hbridoma protein that
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                             Ig heavy chain V region pe22 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S5538
C;Accession: S5538
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
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R;Caton, A.J.; Brownlee,
EMBO J. 5, 1577-1587, 19
A;Title: Structural and
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A;Residues: 1-120 <BOE>
A;Cross-references: EMBL:X82589; NID:g854304; PIDN:CAA57925.1; PID:g854305
A;Cross-references: EMBL:X82589; NID:g854304; PIDN:CAA57925.1; PID:g854305
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>
A; Molecule type: mRNA
A; Residues: 1-120 <BOE>
A; Cross-references: EME
                                                                                                    A; Reference number:
                                                                                                                       A;Title: Comprehensive epitope analysis of utations in the variable region genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig heavy chain V region (H158-89H4) - C; Species: Mus musculus (house mouse)
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                                                             A;Status: preliminary
                                                                                   A;Accession:
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Best Local S
Matches 106
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Best Local :
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                                                                                                      S55528;
  EMBL: X82591;
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88.3%;
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                                                                                                        MUID:95239763;
  NID:g854308;
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Pred. No. 7.1e-31;
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                                                                                                        PMID: 7536850
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  PIDN:CAA57927.1; PID:g854309
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A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin utations in the variable region genes.
A;Reference number: $55528; MUID:95239763; PMID:7536850
A;Accession: $55539
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <BOE>
                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region pe24 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #te
C;Accession: S5539
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
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A;Molecule type: mRNA
A;Residues: 1-120 <BOE>
A;Residues: 1-120 <BOE>
A;Cross-references: EMBL:X82590; NID:g854306; PIDN:CAA57926.1; PID:g854307
A;Cuperfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>
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A;Accession: S55537
A;Status: preliminary
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C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S5537
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
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                                                                                     A,Cross-references: EMBL:X82593; NID:g854312; PIDN:CAA57929.1; PID:g854313 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords : heterotetramer; immunoglobulin C;Keywords : heterotetramer; immunoglobulin F;14-97/Domain: immunoglobulin homology <IMM>
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Score 532; DB 2;
Pred. No. 3.5e-30;
8; Mismatches 8
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Pred. No. 3e-30;
7; Mismatches. 8
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Pred. No. 3e-30;
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VKLVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGSYTYYP

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                                                                                                                                                                                                                                                                                                                                           Ig heavy chain V region (H35-C6) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: E27888
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A;Residues: 1-548 <KIP>
A;Residues: 1-548 <KIPA
A;Cross-references: EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PID:g940782
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;353-421/Domain: immunoglobulin homology <IVM>
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submitted to the EMBL Data Library, Nove
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S38864
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                                                                                                                 C;Superfamily: immunoglobulin V region; imm C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IV
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A; Residues: 1-122 < CAT>
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A; Accession: S38864
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001
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VKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTTYP 61
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                                                Conservative
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                                                              41.7%;
85.1%;
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Pred. No. 1.7e-29;
6; Mismatches 22
                                            Score 530; DB 2;
Pred. No. 4.9e-30;
5; Mismatches 9
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A; Molecule type: mmNA
A; Residues: 1-112 <STA>
A; Cross-references: EMBL: X59192
C; Superfamily: imm:noclot.
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C;Accession: B31790
R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, J. Biol. Chem. 263, 17100-17105, 1988
A;Title: Preliminary crystallographic data, primary sequence, and binding data for A;Reference number: A92686; MUID:89034213; PMID:3182835
A;Accession: B31790
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                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region - mouse (fragment)
c;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C;Accession: S26327
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A; Residues: 1-254 < SCH>
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Matches 102
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Best Local S
Matches 107
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                                                                                                                                                                                                        9-91/Domain:
                                                                                                                                                                                                                  Superfamily: immunoglobulin V region; immunoglobulin Keywords: heterotetramer; immunoglobulin
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Species: Mus musculus (house mouse)
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                                                                          S 122
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              RFTISRDNARNILYLQMSSIRSEDTAMYYCARLYGNY--WYFDVWGAGTTVTVSS
                                RFTISRDNAKNTLYLQMSSLKSEDTAMYYCAR--GNWEGWYFDVWGQGTTVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGSGGGGGGSNIELTQSPAIMSASP-----GERVTMTC 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDSVKGRFTISRDNAKNTLYLOMSSLKSEDSAMYYCARRERYDENGFAYWGQGTLVTVSA 120
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                                                                                                                                                                                                     immunoglobulin homology <IMM>
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llarity 88.7%;
Conservative
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Pred. No. 3.7e-29;
3; Mismatches 20
                                                                                                                                       Score 520.5; DB
Pred. No. 2e-29;
5; Mismatches
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A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0249
A;Molecular terms of the second second
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(;Species: Mus musculus (house mouse)
(;Species: Mus musculus (house mouse)
(;Date: 16-Rep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
(;Accession: PL0249
(;Accession: PL0249
(;Accession: PL0249
(;Accession: M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: I27887
R;Caton, A.J.; Brownlee, G
EMBO J. 5, 1577-1587, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (H37-45) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-121 < CAT >
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F;109-117/Region:
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A; Residues: 1-117 < SHL>
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Best Local S
Matches 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Keywords:
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ain: immunoglobulin homology <IN
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S 118
                                                                            PDSVKGRFTISRDNAKNTLYLQMSRLRSEDTAMYYCAREEGLRLEDYAMDYWGQGTSVTV
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83.8%;
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y-determining 1
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Pred. No. 5.7e-29;
6; Mismatches 12
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Pred. No. 2.3e-29;
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121 8 121

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Ig heavy chain V region (anti-DNA, clones 2E3VH, 688VH, and 3G9VH) - mouse (fragment)
C;Species: Mis musculus (house mouse)
C;Satc: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C;Accession: PL0252; FL0251
C;Accession: PL0252; FL0251
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Reference number: FL0231; MOID:90111618; PMID:2104919
A;Accession: PL0252
A;Mccession: FL0231; MOID:90111618; PMID:2104919
A;Mccession: FL0232
A;Mclecule type: mRNA
A;Residues: 1-117 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin homology 

C;Mccession: FL0232
C;Superfamily: immunoglobulin homology
C;Superfamily:
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Minimum
Maximum
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Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      protein search,
                                                                                                                                                                                       length:
A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp20018:*
5: geneseqp2002s:*
6: geneseqp2003bs:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
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Gapop 10.0 , Gapext 0.5
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513.066 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                           US-10-073-301A-2
                                                                                                                                 Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                         2002273 seqs, 358729299 residues
                                                                                                                                                                                                                                                                                                                               IMDQVPFSV 9
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           geneseqp1980s:*
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	_U	4.	ω	N	٦	Result No.
45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	Score
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25	25	20	20	20	20	20	17	17	17	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	Length
4.	4	v	v	4	4	4.	4.	4	4	7	7	σ	σ	σ	0	0	σ	5	ຫ	4	4	4	4	N	B
AAU72232	AAU72228	AAE13456	AAE13455	AAU72229	AAU72224	AAU72223	AAU72231	AAU72226	AAU72227	ADB97733	AAE38651	ADA89157	ABU08668	ABJ19877	AAE35575	AAG79857	AAE36055	AAE17297	AAO17085	AAE05120	AAU10221	AAU72002	AAU28966	AAR84817	ID
Aau72232 gp100-der	Aau72228 gp100-der	6 Humar	Aae13455 Human gpl	Aau72229 gp100-der	Aau72224 gp100-der		Aau72231 gp100-der	Aau72226 gp100-der	Aau72227 gp100-der	Adb97733 Human gpl	Aae38651 HLA-A2 re	Ada89157 Gp100-der		Abj19877 MHC bindi		Aag79857 HLA-A2-re	Aae36055 Tumour as		Aao17085 Gp 100 an	Aae05120 Modified	Aau10221 Cancer ce	Aau72002 gp100 mel		7 Modif	Description

45	. 44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	
39	39	39	39	41	41	41	41	41	42	42	42	45	45	45	45	45	45	45	
86.7	86.7	86.7	86.7	91.1	91.1	91.1	91.1	91.1	93.3	93.3	93.3	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
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AAW78851	AAW54599	AAW70018	AAR84210	ADB97734	AAB98098	AAB97708	AAU28967	AAR84818	ADB97732	AAU28965	AAR84816	AAB98206	AAE05116	AAB97816	AAE35578	AAE13457	AAU72225	AAU72230	
Aaw78851	Aaw54599	Aaw70018	Aar84210	Adb97734	Aab98098	Aab97708	Aau28967	Aar84818	Adb97732	Aau28965	Aar84816	Aab98206	Aae05116	Aab97816	Aae35578	Aae13457	Aau72225	Aau72230	
PMEL 1	Peptide	Melanoma	gp100 me.	Human 91		Avipox vi	Modified	Modified	Human gp	Modified	Modified	Human gpi	Modified	Modified	TA pepti	Human gr	gp100-der	gp100-der	

ALIGNMENTS

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RESULT 1
AAR84817
22-APR-1994;
05-APR-1995;
                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                          diagnosis; prognosis; prophylaxis; therapy; vaccine
                                                                                                                                                                                                                                                  MART-1; M9-2; melanoma antigen recognised by T-cells; melanoma; metastatic melanoma; tumour-associated antigen; immunogenic peptide;
                                                                                                                                                                                                                                                                        Modified gp100
                                                                                                                                                                                                                                                                                                     AAR84817;
                                                                                                                                                                                                                                                                                                                   AAR84817 standard; peptide; 9
                                                                                                                                                                                  21-APR-1995;
                                                                                                                                                                                                02-NOV-1995.
                                                                                                                                                                                                               WO9529193-A2.
                                                                                                                                                                                                                                                                                       25-APR-1996
                                                                                                                                              (USSH ) US SEC DEPT HEALTH.
                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                        melanocyte-melanoma specific antigenic peptide G9-209-2M.
                                                                                                                                                           94US-00231565.
95US-00417174.
                                                                                                                                                                                  95WO-US005063
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Kawakami Y, Rosenberg SA;

WPI; 1995-382963/49.

DNA encoding melanoma antigens recognised by T-lymphocytes - also vectors, host cells and antibodies, used to detect, treat and immu animal against melanoma. and immunise

Example 5; Page 107; 184pp; English.

AAR84816-836 are G9-209 peptides modified to improve immunogenicity. G9-209 is an immunogenic peptide based on the melanoma derived antigen, g100 (see AAR84210). The peptides are used in medicaments for the treatment or prevention (by immunization) of melanoma. Antibodies against MART-1 and its immunogenic peptides may be used in the detection and isolation of MART-1 from a sample, the detection of which is indicative a disease state (melanoma 유 metastatic melanoma

Sequence 9 AA;

Query Match

100.0%; Score 45; DB <u>د.</u> Length 9

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RESULT 3
AAU72002
ID AAU7
XX
AC AAU7
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AC AAU7
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Matches 9
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                                                                                                                                                                                                                                                                                                                                               22-APR-1994;
05-APR-1995;
05-MAY-1998;
                                                                                                                                                                              The invention relates to a novel immunogenic peptide comprising 5-2 contiguous amino acids of new melanoma antigen recognised by T lymphocytes (MART-1). The peptide sequence contains at least one an acid modification of MART-1. The peptide is used in diagnostic and therapeutic methods as an immunogen or vaccine to prevent or treat melanoma, and for in vivo tumour recognition and rejection. AAU280 AAU29008 represent MART-1 peptide amino acid sequences, and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; MART-I; immunogenic; melanoma antigen recognised by T lymphocyte; diagnostic; therapeutic; vaccine; melanoma; in vivo tumour recognition; in vivo tumour rejection.
                                                                                                                                                        Sequence 9
                                                                                                                                                                                                                                                                    Immunogenic peptide useful in vaccines comprises specific amino acids new melanoma antigen recognized by T lymphocytes.
         26-FEB-2002
                           AAU72002;
                                          AAU72002 standard;
                                                                                                                                                                                                                                                   Example 5;
                                                                                                                                                                                                                                                                                                              Kawakami Y,
                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU28966 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN
                                                                                                                     Local Similarity nes 9; Conserv
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                                                                                    IMDQVPFSV
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                                                                                                                                                        AA,
                                                                                                                                                                                                                                                   Col 55; 73pp; English.
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                              Rosenberg SA;
         (first entry)
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                                                                                                                                                                                                                                                                                                                                              94US-00231565.
95US-00417174.
98US-00073138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G9-209 peptide
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                                                                                                                                                                         invention
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                                         peptide;
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Pred. No. 1.7e+06;
; Mismatches 0;
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RESULT 4
AAU10221
ID AAU1
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AC AAU1
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CANC
DB CANC
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KW Huma
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WO20
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising administration of an immunotherapeutic composition, comprising a heat shock protein, and a melanoma antigen, where the melanoma antigen is selected from tyrosinase, tyrosinase related protein 1, tyrosinase related protein 2, gp 100, MAGE antigens, BAGE antigens, NYES01, MART antigens, GM2, antigenic portions and combinations of these. The melanoma antigen is covalently bound to a javelin molecule, where the melanoma antigen bound to the javelin molecule is non-covalently bound to the heat shock protein. The composition is useful for inducing an immune response for the treatment of melanoma. AAU71980-AAU72481 represent melanoma
                                                                                               Human; cancer cell associated peptide; G9-209-2M; CTL; single chain major histocompatibility complex class I; human beta-2 microglobulin; cytotoxic T lymphocyte; car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Melanoma antigen; MART-1; MAGB-1; gpl00; cytostatic; immune response; immunotherapeutic; heat shock protein; tyrosinase; BAGE; NYBE01; GM2; tyrosinase related protein 1; tyrosinase related protein 2; vaccine; javelin molecule; melanoma antigen recognised by T cells-1; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9
                                                                                                                                                                                   Cancer cell associated peptide G9-209-2M.
                                                                                                                                                                                                                               27-FEB-2002
                                                                                                                                                                                                                                                                      AAU10221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen peptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of induction of an immune response,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 11; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti cancer vaccine for the treatment of melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-663092/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Houghton A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2001.
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LIVINGSTON P.
AL-AWQATI Q.
MAYHEW M.
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                                                                                                                                                                                                                                                                                                               peptide;
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Pred. No.
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                                                                                                   complex class I; MHC; T lymphocyte; cancer.
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WO200172768-A2

Homo sapiens.

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RESULT 5
AAE05120
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a recombinant single chain major histocompatibility complex (MHC) class I polypeptide comprising an amino acid sequence including a functional human beta-2 microglobulin (in)directly covalently linked to a functional human MHC class I heavy chain and the nucleic acids encoding it. The recombinant MHC polypeptide is used in a method is for generating large quantities of pure single chain MHC class I polypeptides, which is useful in monomeric or multimeric forms to present antigenic peptides to cytotoxic T lymphocyte (CTL) clones. The present sequence is a cancer cell associated peptide which can bind MHC in an experiment demonstrating the production of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New major histocompatibility complex (MHC) class I polypeptide, useful for presenting antigenic peptides to cytotoxic T lymphocyte clones, comprises beta-2 microglobulin covalently linked to MHC class I heavy
Emtage
                                                    05-JAN-2000; 2000US-0174587P
                                                                              05-JAN-2001; 2001WO-CA000005
                                                                                                                                      WO200149317-A2
                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                               vaccine; cancer;
                                                                                                                                                                                                                                                         Tumour-associated antigen; TAA; GP100 antigen; cytostatic; gene therapy; immune response; tetanus toxoid; TT; diphtheria toxoid; DT; prophylactic;
                                                                                                                                                                                                                                                                                                   Modified tumour-associated antigen, GP100 peptide, CLP 572
                                                                                                                                                                                                                                                                                                                               18-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                 AAE05120 standard; peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant
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                                                                                                           12-JUL-2001.
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                           (AVET ) AVENTIS PASTEUR LTD.
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 Barber BH,
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                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                              note= "Wild type Thr substituted with Met"
                                                                                                                                                                                                                                            therapeutic
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 Sambhara
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Pred. No. 1.7e+06;
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 GY;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enhancing immune response to antigen such as tumor antigen for t
cancer in an animal involves administering an inducing agent to
animal followed by administering inducing agent-antigen mixture.
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The present invention relates to a method for the preparation of ready-for-use, cryopreserved, mature dendritic cells comprising growing immature dendritic cells in a culture medium that includes a 'maturation cocktail' of one or more maturation stimuli and freezing the resulting matured cells in a freezing medium that does not contain heterologous serum. When loaded with antigens, the dendritic cells can be used as
                                                                                                                                                          Preparation of cryopreserved, mature dendritic cells, useful in vaccines, comprises culturing immature cells on medium containing cocktail of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virucide; cancer; hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cryopreserved mature dendritic cell; antigen; vaccine; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gp 100 analogue antigen SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAO17085 standard; peptide;
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                                                                                                             Disclosure; Fig 28; 87pp;
                                                                                                                                             maturation factors,
                                                                                                                                                                                                           WPI; 2002-292062/33
                                                                                                                                                                                                                                          Schuler G,
                                                                                                                                                                                                                                                                                                         24-AUG-2000; 2000DE-01041515
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                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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The present invention relates to an artificial antigen presenting cell (AAPC) comprising a eukaryotic cell expressing an antigen presenting complex comprising beta2-microglobulin, an exogenous accessory molecule, complex comprising beta2-microglobulin, an exogenous accessory molecule, complex complex presenting cell and a protein that is processed intracellularly complex produce an exogenous T cell-specific epitope. The invention also cellates to methods for activation of T lymphocytes. The method is also cellates to methods for activation of T lymphocytes. The method is also cellates (CTLs), which is useful for diagnostic purposes. AAPC is specific antigen (TCA), which is useful for diagnostic purposes. AAPC is also useful for activating CTLs, by contacting AAPC with a suitable compulation of T lymphocytes under conditions suitable for the activation of T lymphocytes under conditions suitable for the activation of primary T cell activation and diagnostic applications cellated primary T cell activation and diagnostic applications cellated primary T cell activation and diagnostic applications and cessory consistency immune response in normal, infected or treated (vaccinated) patients. Composition comprising AAPC or activated T cells produced by cutilising AAPC is useful for eliciting an antitumour response. The convention is used for the treatment of cancer. The present sequence is gp
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Artificial antigen presenting cells for activating T lymphocytes, comprises eukaryotic cell expressing antigen presenting complex having beta2-microglobulin, exogenous accessory molecule, human leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Artificial antigen presenting cell; AAPC; beta2-microglobulin; human leukocyte antigen; HLA; major histocompatibility complex; MHC; cytotoxic T lymphocyte; CTL; T cell-specific antigen; TCA; antitumour; immune response; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gp100-modified peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                         Example 7; Page 29; 75pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sadelain M,
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9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                             molecule and protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           against tumours and hepatitis B virus. The present antigen described in the invention
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RESULT 8
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                                                                                                                                The invention relates to immuno-molecules comprising a soluble human major histocompatibility complex (MHC) class I effector domain and a targetting domain linked to the effector domain, useful for immune deception. The invention also relates to methods for immune deception. The method is useful for producing an immunomolecule, and selectively killing a cell in a patient. The immuno-molecules are useful for immune deception, particularly treating cancer. The immuno-molecules and methods are useful for recruiting active cycotoxic T cells for tumour killing via cancer-specific antibody or ligand guided targetting of single-chain MHC-peptide complexes. The present sequence is a tumour associated HLA-A2-restricted peptide used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                             New immuno-molecules comprising a soluble human major histocompatibility complex class I effector domain and a targeting domain linked to the effector domain, useful for immune deception, particularly in treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9
                                                                                                          Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-2001; 2001US-0298915P.
29-MAR-2002; 2002US-00108511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Major histocompatibility complex; MHC; immune deception; cytostatic; therapy; cytotoxic T cell; immunostimulant; cancer.
                                                                                                                                                                                                                                                                                                      Example; Page 50; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-210086/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour associated HLA-A2-restricted peptide, G9-209-2M
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IMDQVPFSV
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Pred. No. 1.7
0; Mismatches
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RESULT 9

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RESULT 10
AAE35575
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carcinoembryonic antigen. The human T cell clones which are generated were used in the method of the invention for treating cancer, such as haematological cancer, neurological cancer, melanoma, breast cancer, cancer, head and neck cancer, gastrointestinal cancer, genitourinary cancer, bone cancer or vascular cancer, or infections by influenza v. HIV, M. tuberculosis, or P. falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enhancing T cell responsiveness in a mammal, useful for treating cancer or other infections, comprises administering to the subject a compound comprising an agent that interferes with an interaction between B7-H1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-067637/06.
                             Melanoma gp100 eptiope
                                                                                           17-JUN-2003
                                                                                                                                                                                                                  AAE35575 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-APR-2001; 2001US-0285137P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M. tuberculogis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA-A2-restricted epitope of the gp100 melanoma antigen.
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9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
larity 100.0%;
Conservative (
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                                                                                        (first entry)
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Pred. No. 1.7e+06;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is an HLA
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RESULT 11
ABJ19 ABJ19
XX ABJ19
AC ABJ19
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AC ABJ19
XX ANTI:

MHC binding

peptide SEQ ID

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42.

10-APR-2003

(first entry)

ABJ19877 standard; peptide;

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28-NOV-2002 WO200294981-A2 Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective; antiinflammatory; major histocompatibility complex; MHC; autoimmune disease; T cell; B cell; allergic disease; multiple sclerosi rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease; inflammation; gene therapy; MHC binding peptide.

multiple sclerosis;

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Query Match Best Local S Matches

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CC The invention relates to a fusion agent (Trojan antigen; TA) comprising a CC transport domain, two cleavage sites, a peptide epitope recognised by an CC antigen-specific receptor on an effector T-lymphocyte precursor cell and CC a biologically active agent, where there is a cleavage site between the CC peptide epitope and the biologically active agent and between the CC biologically active agent. The fusion agent is used to make a cell immunogenic or antigenic. It is also useful for preventing and treating CC naminfectious disease such as viral, bacterial, protozoal, fungal or CC yeast disease, or proliferative disease such as cancer (e.g. melanoma, CC neural tissue, gastrointestinal, breast, lung, ovarian, testicular, cervical, bladder, vaginal, liver, renal, bone, haematological CC prostate, cervical, bladder, vaginal, liver, renal, bone, haematological CC prosent sequence is melanoma agplo0 eptiope. This peptide is used in the CC present sequence is melanoma agplo0 eptiope. This peptide is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion agent useful for preventing and treating an infectious disease, a proliferative disease, such as cancer, comprises a transport domain, two cleavage sites, a peptide epitope and a biologically active agent.
                                                                                                                                                                                                      Sequence 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 37; 72pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion agent; immunogenic; proliferative disease; infectious disease; cancer; therapy; vaccine; melanoma; Trojan antigen; TA; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-140367/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MAYO-) MAYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAY-2002; 2002WO-US015992
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1 IMDQVPFSV 9
                                                                        Similarity 9; Conserv
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                                                                               Conservative
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                                                              100.0%; 5c.
100.0%; Pr
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                                                                                                         Score 45;
Pred No.
                                                                               Mismatches
                                                              DB 6;
1.7e+06;
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Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel method for identifying peptides originating from a particular cell type, which are capable of binding to major histocompatibility complex (MHC) molecules of a particular haplotype. The method comprises analysing peptides bound to the soluble and secreted form of the MHC molecules of the particular haplotype. The method is useful for identifying peptides for treating an autoimmune disease, such as T or B cell and/or allergic disease or condition, rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders, e.g. Alzheimer's disease, or diseases associated with inflammation. The sequences of the invention may be used in a gene therapy application.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric polypeptide; antigenic peptide; MHC class I; major histocompatibility complex class I, beta-2 microglobulin; MHC class I; crycotoxic T-lymphocyte; MHC binding T cell epitope; primary CTL induction; melanoma antigen gp100; cancer; G9-209-2M.
      WPI; 2003-352830/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying peptides that are capable of binding to major histocompatibility complex (MHC) molecules of a particular haplotype by analyzing peptides bound to the soluble and secreted form of the MHC molecules of the particular haplotype.
                                                                  Reiter
                                                                                                                                                                                                                                                                                                                                                                         US2003003535-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cancer cell associated peptide G9-209-2M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU08668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9
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29-MAY-2001; 2001US-00865548.
                                                                                                                           (TECR ) TECHNION RES & DEV FOUND LTD
                                                                                                                                                                                        27-MAR-2000; 2000US-00534966
                                                                                                                                                                                                                                             13-FEB-2002; 2002US-00073300
                                                                                                                                                                                                                                                                                                             02-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s sequence represents a peptide relating to the method for identifying binding peptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M
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Similarity 100.0%;
9; Conservative 0
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 6; I
. 1.7e+06;
ches 0;
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RESULT 13
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a chimeric polypeptide (I) comprising an antigenic peptide capable of binding a human major histocompatibility complex (MHC) class I, a functional human beta-2 microglobulin and a functional human MHC class I heavy chain. The chimeric polypeptide is useful in generating large quantities of pure single chain MHC class I polypeptides which can be used in monomeric or multimeric form to present antigenic peptides to cytotoxic T-lymphocyte (CTL) clones. They may also be used in rapid, sensitive and reliable MHC peptide binding assay to identify high affinity MHC binding T cell epitopes, in in vitro primary CTL induction studies to define those peptides that are immunogenic, and to generate antibodies. This is the amino acid sequence of a cancer cell associated peptide derived from melanoma antigen gp100 and used for major histocompatibility (MHC) binding
                                                                                                                                                                                                                                                                                                                                                                                                              immunoglobulin; Ig; heavy chain variable domain;
light chain variable domain; major histocompatibility complex; MHC;
gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9
                                                                                                                                                                                                                              20-FEB-2002; 2002US-0358994P
                                                                                                                                                                                                                                                                                           28-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gp100-derived peptide G9-209 SEQ ID NO:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigenic peptide that binds a human major histocompatibility complex (MHC) class I, a human beta-2 microglobulin and a human MHC class I heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New chimeric polypeptide useful for generating antibodies, comprises an antigenic peptide that binds a human major histocompatibility complex
                                                                                                                    WPI; 2003-663847/62.
                                                                                                                                                   Hoogenboom HRJM, Reiter Y;
                                                                                                                                                                                                                                                            20-FEB-2003; 2003WO-US005128
                                                                                                                                                                                                                                                                                                                        WO2003070752-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA89157 standard; peptide; 9
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                                                                                                                                                                                RES & DEV FOUND
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Pred. No. 1.7e+06;
; Mismatches 0;
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New protein comprising an immunoglobulin heavy chain variable and an immunoglobulin light chain variable (VL) domain, useful preparing a composition for treating or preventing a cancerous

a cancerous

(VH) domain disorder.

The present invention describes a protein comprising an immunoglobulin

Claim 4; Page 137; 224pp; English

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RESULT 14
AAE38651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL) CC domain. The protein binds a complex comprising a major histocompatibility CC complex (MHC) and a peptide, does not substantially bind the MHC in the CC absence of the bound peptide, and does not substantially bind the peptide CC in the absence of the MHC. The peptide is a peptide fragment of gpl00, CC MUC1, TAX or hTERT. ALSO described: (1) a pharmaceutical composition CC comprising the novel protein and a carrier; (2) a cytocoxic T cell CC comprising an MHC and a peptide, does not substantially bind the MHC complex having an MHC and a peptide, does not substantially bind the MHC comprising a first segment that encodes the Ig variable domain; (4) a CC comprising a first segment that encodes the Ig variable domain; (4) a CC comprising heterologous nucleic acid sequences that encodes the cell comprising heterologous nucleic acid sequences hat encodes the protein; (5) a transgenic animal whose genome includes heterologous nucleic acid sequences that encodes the protein; (6) identifying the CC protein that specifically binds the MHC-peptide complex; (7) expressing CC an antigen-binding protein; (8) ablating or killing a target cell that clipbays a peptide on a surface MHC molecule; (9) treating or preventing CC complex in a sample. A protein of the invention has cytostatic activity, and can be used in gene therapy. The protein is useful for preparing a CC composition for treating or preventing a cancerous disorder. The present cc exemplification of the present invention.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Major histocompatibility complex; MHC; HLA-restricted antigen; cancer; viral infection; autoimmune disease; gene therapy; cytostatic; virucide; immunomodulator.
New isolated molecule comprising an antibody that binds with a human major histocompatibility complex (MHC) class I being complexed with a restricted antigen, useful for treating cancer, viral infection or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                     11-FEB-2003; 2003WO-IL000105
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                                                                                                                                                               WPI; 2003-689603/65.
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Pred. No. 1.7e+06;
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Example;

Page 10; 81pp; English

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                                                   The invention relates to an immunogenic peptide having contiguous amino acids derived from the sequence of melanoma antigens recognised by T-lymphocytes (MART-1) or gpl00. The MART-1 sequence appears as ADB97651, and the gpl00 (differing by 1 amino acid from the previously published gpl00 (ADB97770) appears as ADB97676. Also included are a pharmaceutical composition (comprising the above peptide and a excipient, diluent or carrier), a vaccine for immunising a mammal (comprising the above peptide in a carrier), preventing or treating melanoma (comprising administering the above composition to a mammal in an amount to stimulate the production of protective antibodies or immune the stimulate the production acid sequence encoding the above peptide, a recombinant expression vector comprising at least one nucleic acid sequence cited above, a host organism transformed or transfected with the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; melanoma antigen recognised by T-lymphocytes; MART-1; melanoma; skin cancer; T lymphocyte; cytostatic; gene therapy; vaccine; antigen; major histocompatibility complex; MEC; human leukocyte antigen; HLA-A2; tumour infiltrating lymphocyte; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New immunogenic peptides derived from melanoma antigens recognized by lymphocytes or from gp100, useful for preventing or treating melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kawakami Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-APR-1994;
12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Page 31; 77pp; English.
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99US-00267439.
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and antibodies reactive with peptide sequence contains
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Pred. No. 1.7
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CC acid modification (amino acid substitution) of the MART-1 or gp100 CC sequence to enhance binding of the peptide to a Major Histocompatibility CC complex (MHC) molecule. The peptide is recognised by Human Leukocyte CC Antigen (HLA)-A2 restricted tumour infiltrating lymphocytes. The CC composition and methods are useful in preventing or treating melanoma and skin cancer. The present sequence represents a modified melanoma and CC antigenic peptide of the invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 45; DB 7; Length 9; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IMDQVPFSV 9 | DB 1 IMDQVPFS
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
         protein search, using
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Match
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Gapop 10.0 , Gapext 0.5
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Query Match Best Local Similarity Matches 8; Conserva	RESULT 2 A49179 A49179 melanoma antigen homolog rp. C;Species: Bos primigenius C;Date: 19-Dec-1993 #sequen C;Accession: A49179; I45861 R;Kim, R.Y.; Wistow, G.J. Exp. Eye Res. 55, 657-662, A;Title: The cDNA RPE1 and 1 A;Reference number: A49179; A;Accession: A49179 A;Accession: A49179; A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-491 <kim>A;Essidues: 1-491 <kim>A;Cross-references: UNIPROT A;Experimental source: reti A;Note: sequence extracted C;Genetics: A;Gene: RPE1</kim></kim>	RESULT 1 T16581 T16581 T16581 T16581 T16581 C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T16581 R;Pauley, A. submitted to the EMBL Data Library, A;Description: The sequence of C. e A;Reference number: Z18541 A;Accession: T16581 A;Access	30 31 68.9 31 31 68.9 32 31 66.7 34 30 66.7 35 30 66.7 37 30 66.7 38 30 66.7 40 30 66.7 41 30 66.7 42 30 66.7 43 30 66.7 44 30 66.7 45 30 66.7 46 30 66.7
86.7%; Score 39; DB 2; 88.9%; Pred. No. 3.5; rative 0; Mismatches	pel - bovine (fragme) taurus (cattle) nce_revision 18-Nov- 1 1992 monoclonal antibody , MUID:93122163; PMI T:006154 inal pigment epithel from NCBI backbone	orhabditis elvion 20-Sep-19: ion 20-Sep-19: October 1995 legans cosmid rom GB/EMBL/DI EMBL:U38377; ol N2 core 40; DB: red. No. 1.1; Mismatches	770 2 S11161 837 2 157557 848 2 157547 126 2 S77183 156 2 149446 200 2 E81314 248 2 B93134 263 2 E75046 319 2 D97205 318 2 D75353 389 2 H90413 390 2 A10396 410 2 T38815 455 2 T32189 474 2 T29336 482 2 T43996 ALIGNMENTS
Length 491; 1; Indels 0; Gaps	<pre>#text_change 09-Jul-200 -50 define gene products 78275</pre> IN:122438, NCBIP:122439)	<pre>gans 99 #text_change 09-Jul-2004 K08A8. NID:g1022968; PID:g1022970; NID:g1022968; PID:g1022970; NID:g1022968; PID:g1022970; NID:g1022968; PID:g1022970;</pre>	anthranilate synth DNA-Binding Protei interleukin-4-indu hypothetical prote 8-0x0-dGTPase - mo probable pili asem probable pili asem hypothetical prote hypothetical prote yellow-related proconserved hypothet multidrug resistan septin homolog spn zinc finger protei hypothetical protei typothetical protei finger protei hypothetical protei multidrug resistan septin homolog spn zinc finger protei hypothetical protei hypothetical protei virion protein [im
0;	preferential	PIDN:AAA79	tei tei ndu ote mo ote sam sem sem ote ote ote ote ote fin

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A; Molecule type: mRNA
A; Residues: 1-592,594-662 < ADB>
A; Residues: 1-522,594-662 < ADB>
A; Residues: 1-522,594-662 < ADB>
A; Kawakami, Y.; Ellyahu, S.; Delgado, C.H.; Robbins, P.F.; Sakaguchi, K.; Appella, E. Proc. Natl. Acad. Sci. U.S.A. 91, 6458-6462, 1994
A; Title: Identification of a human melanoma antigen recognized by tumor-infiltrating A; Reference number: A55753; MUID:94294401; PMID:8022805
A; Accession: A55753
A; Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-662 <RES>
A;Cross-references: UNIPROT:P40967; EMBL:U01874; NID:g494939; PIDN:AAA18479.1; A;Cross-references: UNIPROT:P40967; EMBL:U01874; NID:g494939; PIDN:AAA18479.1; R;Adema G,J.; de Boer, A.J.; Vogel, A.M.; Loenen, W.A.M.; Figdor, C.G. J. Biol. Chem. 269, 20126-20133, 1994
A;Tittle: Molecular characterization of the melanocyte lineage-specific antigen A;Reference number: A33668; MUID:94327568; PMID:7519602
A;Accession: A53668
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C;Date: 01-Nov-1996 #text_change
C;Date: 01-Nov-1996 #sequence revision 01-Nov-1996 #text_change
C;Accession: 13840; A53668; A55753
R;Maresh, G.A.; Marken, J.S.; Neubauer, M.; Aruffo, A.; Hellstro
DNA Cell Biol. 13, 87-95, 1994
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A;Title: Mouse silver mutation is caused by a single base insertion in the putative cytc A;Reference number: S53871; MUID:95175358; PMID:7870580
A;Accession: S53871
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C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence revision
C;Accession: I38400; A53668; A55753
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C;Species: Mus musculus (house mouse)
C;Date: 27-Oct_1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
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A; Residues: 1-626 < KWO>
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Residues: 1-161,'F',163-592,594-662 <KAW>
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;Reference number: I38400; MUID:94235165; PMID:8179825
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0; Mismatches
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Pred. No. 4.6;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-350 <RES>
A;Cross-references: UNIPROT:P53670; GB:D31876; NID:g1684614; PIDN:BAA06675.1; PID:g1000:F;51-103/Domain: LIM metal-binding repeat homology <LIM2>
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(;Species: Rattus norvegicus (Norway rat)

(;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996

C;Accession: I78848

C;Accession: I78844, K.; Okano, I.; Mizuno, K.

R;Nunoue, K.; Ohashi, K.; Okano, I.; Mizuno, K.

Oncogene 11, 701-710, 1995

A;Title: LIMK-1 and LIMK-2, two members of a LIM mo
                                                                                                                                                                                                                                                                                                                                                                                                 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C. C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Nature 403, 665-668, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Cj1454c [imported] - Campylobacter jejuni (strain NCTC C;Species: Campylobacter jejuni (strain NCTC C;Species: Campylobacter jejuni (strain NCTC C;Date: 3)-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: E81291
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E81291
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A;Accession: A41234
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A41234
                                                                                                         A; Cross-references: UNIPROT: Q9PMK6; A; Experimental source: serotype O2,
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   A;Gene: Cj1454c
C;Superfamily: (
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A; Residues: 1-668 < KWO>
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C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 30-Sep-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 VQDQLPYSV 129
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hypothetical
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Pred. No. 4.9;
0; Mismatches
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Pred. No.
                                                                                                             GB:AL139078; GB:AL111168; strain NCTC 11168
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protein b0835
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A;Cross-references: UNIPROT:054785; DDBJ:AB008119
A;Experimental source: embryo
C;Comment: This care
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A;Title: LIMK-1 and LIMK-2, two members of a LIM motif-containing
A;Reference number: IS8353; MUID:95380177; PMID:7651734
A;Accession: I78847
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references:
C;Genetics: <RES1>
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R;KOshimizu, U.; Takahashi, H.; Yoshida, M.C.; Nakamura, T.
Biochem. Biophys. Res. Commun. 241, 243-250, 1997
A;Title: cDNA cloning, genomic organization, and chromosomal
A;Reference number: JC5813; MUID:98086337; PMID:9425257
A;Accession: JC5814
                                                                                                                                                                                                                                                                                                                                       LIM motif-containing protein kinase (EC 2.7.1.-) 2, splice form C; Species: Mus musculus (house mouse)
C; Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change
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                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-617 < KOS>
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A; Residues: 1-163 < RE2>
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       .Map position: 1d
.Map position: 1d
.Superfamily: LIM protein kinase; LIM metal-binding repeat
.Keywords: alternative splicing; phosphotransferase
.Keywords: alternative splicing; phosphotransferase
.751-103/Domain: LIM metal-binding repeat homology <LIM2>
.700 E07/Domain: protein kinase homology <KIN>
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                                                                                                       ;Gene: Limk2b
                                                                                                                                                                                                                        Status: nucleic acid sequence
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 317-580/Domain: protein kinase
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6; Conserv
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5; Conserv
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is involved in a signal transduction
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75.0%;
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Pred. No. 56;
1; Mismatches
 #status predicted
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Pred. No.
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82;
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C; Superfamilia
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Oncogene 11, 701-710, 1995
A;Title: LIMK-1 and LIMK-2, two members of
A;Reference number: I58353; MUID:95380177;
A;Accession: I78846
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A;Experimental source:
C;Comment: This enzyme
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A; Residues: 1-638 < KOS>
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A; Residues: 1-638 < RES>
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Best Local S
Matches 5
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C;Accession: JC5813
C;Accession: JC5813
R;Koshimizu, U.; Takahashi, H.; Yoshida, M.C.; Nakamura, Biochem. Biophys. Res. Commun. 241, 243-250, 1997
Biochem. Biophys. Res. Commun. carjanization, and chromos A;Title: cDNA cloning, genomic organization, and chromos a:Reference number: JC5813, MUID:98086337; PMID:9425257
                                                                                    C;Kuyerfamily: LIM protein kinase; LIM metal-binding repeat C;Keywords: alternative splicing; phosphotransferase C;Keywords: LIM metal-binding repeat homology <LIM1> F;12-3/Domain: LIM metal-binding repeat homology <LIM2> F;329-608/Domain: protein kinase homology <KIN> F;339-601/Domain: protein kinase #status predicted <PKD>
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C;Species: Glycine max (soybean)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S65051
R;LaFayette, P.R.; Nagao, R.T.; O'Grady, K.; Vierling, E.; Key, J.L.
Plant Mol. Biol. 30, 159-169, 1996
A;Fitle: Molecular characterization of cDNAs encoding low-molecular-weight heat shock px A; Heference number: S65049; MUID:96197406; PMID:8616233
                                    low molecular weight heat shock protein precursor (clone Hsp22.5), endoplasmic (;Species: Glycine max (soybean)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: $72398
R;LaFayette, P.R.
submitted to the EMBL Data Library, February 1995
A;Reference number: $72398
A;Accession: $72398
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S65051
A;Status: preliminary A;Molecule type: mRNA
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A; Residues: 1-197 <LAF>
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C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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A;Title: Developmentally regulated Drosophila gene family encoding A;Reference number: A46178; MUID:92409595; PMID:1356269
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;16-107/Domain: fork head DNA-binding domain homology <FHD>
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R.She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, i
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
C90433
ABC transporter, ATP binding protein SSO2600 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
Search completed: December Job time : 5.7561 secs
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C;Superfamily:
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A;Cross-references: UNIPROT:Q39820; EMBL:U21724; NID:g710435; PIDN:AAB03098.1; PID:g7104
                                                                                                                                                                                                                                             A;Cross-references:
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A; Residues: 1-249 < KUR>
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Ś A LO COMPANDA PROPERTA PROPERT Query Match Best Local S Matches 6 Wormbep; KOBAB.2b; CE31200. GO; GO:0003677; F:DNA binding; IEA GO; GO:0006355; P:regulation of tr InterPro; IPR009071; HMG-box. InterPro; IPR009010; HMG 12_box. Pfam; PF00505; HMG box; 1. SMART; SM00399; HMG; 1. PROSITE; PS50118; HMG BOX 2; 1. PROSITE; PS50118; HMG BOX 2; 1. SEQUENCE 199 AA; 22734 MW; D73 Q8IG08; Q8IG08; 01-MAR-2003 01-MAR-2003 01-MAR-2004 01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update Sox (Mammalian sry box) family protein 2, isoform Name=sox-2; ORFNames=KOBAB.2; Waterston Submitted Wilson R.; Submitted (MAY-2003) SEQUENCE FROM N.A. STRAIN-Bristol N2; "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998). SEQUENCE FROM N.A. STRAIN=Bristol N2; MEDLINE=99069613; NCBI_TaxID=6239; Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. EMBL; U38377; AAN72421.1; HSSP; P48432; 1GTO. SEQUENCE FROM N.A. STRAIN=Bristol N2; SEQUENCE FROM N.A. STRAIN=Bristol N2; Submitted Pauley A. Caenorhabditis elegans. Wilson R.; 1 IMDQVPFSV 9 : | | | : | | | : 6; Conserv (OCT-1995) (NOV-2002) Conservative PRELIMINARY; PubMed=9851916; 88.9%; to the ៥ to the EMBL/GenBank/DDBJ databases. the Score 40; DB 2; Pred. No. 2.5; 3; Mismatches EMBL/GenBank/DDBJ databases EMBL/GenBank/DDBJ databases PRT; IEA. D737C6B759ED8944 CRC64; transcription, 199 ₽ update) 0 Length 199; DNA-dependent; IEA. Consortium."; ٥ Indels 0 Gaps

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PIR; T16581; T16581.

HSSP; P48432; 1GT0.

Wormbep; K08A8.2a; CE28595.

GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DN
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InterPro; IPR0090910; HMG-box.

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SMART; SM00398; HMG; 1.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Sox (Mammalian sry box) family protein 2, isoform a.
Name=sox-2; ORFNames=K08A8.2;
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01-MAY-1999 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
Melanocyte protein 17 (F
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
   Eukaryota; Metazoa;
Mammalia; Eutheria;
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STRAIN-Bristol N2;
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STRAIN-Bristol N2;
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01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Melanocyte protein Pmel 17 (Retinal pigment epithelial-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Stricker C., Joerg H., Dummer R., Stranzinger G.; "A comparative genetic approach for the investigation of ageing grey house melanoma.";
                   PROSITE; PS50093; PKD; 1.
Glycoprotein; Melanin biosynthesis; Repeat;
NON TER 1 1 1
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                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a continuous the swiss Institute of Bioinformatics and the EMBL between the Swiss Institute. There are no restrict the European Bioinformatics Institute. There are no restrict the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Exp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93122163; PubMed=1478275; Kim R.Y., Wistow G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                       -!- TISSUE SPECIFICITY: Retinal pigment epithelium.
-!- SIMILARITY: Belongs to the Pmel-17/NMB family.
-!- SIMILARITY: Contains 1 PKD domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=SILV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein) (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000601; PKD.
Pfam; PF00801; PKD; 1.
SMART; SM00089; PKD; 1.
PROSITE; PS50093; PKD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Anim. Breed. Genet. 117:73-82(2000).
EMBL; AF076780; AAC97108.1; -.
                                                                                          Pfam; PF00801; PKD; 1.
SMART; SM00089; PKD; 1.
                                                                                                                                                PIR; A49179; A49179.
                                                                                                                                                                 EMBL; M81193; AAA30419.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The cDNA RPE1 and monoclonal antibody HMB-50 define gene preferentially expressed in retinal pigment epithelium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Retina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
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   TRANSMEM
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                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                             . Eye Res. 55:657-662(1992).
FUNCTION: Could be a melanogenic enzyme (By similarity)
SUBCELLULAR LOCATION: Type I membrane protein (Potentia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
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8; Conserv
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                                                                                                                               IPR000601; PKD.
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88.9%;
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 Potential.
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Matches 8
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Melanocyte protein Pmel 17 precursor (Silver
Name-Silv; Synonyms-Pmel17, D10H12S53E, Si;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Rodentia; Sciurognathi; M
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CARBOHYD
SEQUENCE
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DOMAIN
        PROSITE; PS50093;
Disease mutation;
Transmembrane.
                                                  EMBL; U14133; AAA69538.1; -. PIR; S53871; S53871. MGD; MGI:98301; S1.
                                                                                   or send
                                                                                                     use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                       -!- SIMILARITY: Belongs to the Pmel-17/NMB family.
                                                                                                                                                                                                                                                           Kwon B.S., Halaban R.,
                                                                                                                                                                                                                                                                                                                                                                                      PM17_MOUSE
Q60696;
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                                                                                                                                                                                                                                                                               STRAIN=C57BL/6; TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997
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                                         InterPro; IPR000601; PKD.
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SIMILARITY: Bel
                                 PF00801; PKD;
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174
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                 Glycoprotein; Melanin biosynthesis; Repeat;
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                         PKD; 1.
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N-28BFE5DFBD397D6D CI
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8 X 13 AA approximate to
Potential
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Sciurognathi; Muridae;
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Q9CZB2

ID Q9CZB2

ID Q9CZB2;

AC Q9CZB2;

DT 01-JUN-
E sequence
GN Musmessi
OC Eukaryo
OC Mammali
OX NCBI TA
RN [1] TA
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01-JUN-2001
01-JUN-2001
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DOMAIN
DOMAIN
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STRAIN=C57BL/6J; TISSUE=Whole body;
TNR=21085860; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2811025C24 product:silver, full insert
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REPEAT
                       "Analysis of the mouse transcriptome 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                   the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annot
                                                                                        SEQUENCE FROM N.A.
STRAIN=C57BL/6J; T
                                                                                                                            "Functional annotation of Nature 409:685-690(2001).
                                                                                                                                                                                                                  Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/GJ; TISSUE-Whole body;
STRAINES9727253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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                                                                                       TISSUE=Whole body;
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N-linked (GlcNAc...
N-linked (GlcNAc...
N-linked (GlcNAc...
S->L (in silver).
R->G (in silver).
D->N (in silver).
F->S (in silver).
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Pred. No. 14;
0; Mismatches
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Cytoplasmic
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Extracellular (Potential).
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                                                                                                                                          cDNA collection.";
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Best Local S
Matches 8
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P40967; Q12763; Q14448; Q14817; Q1565;

01-FEB-1955 (Rel. 31, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

05-JUL-2004 (Rel. 44, Last annotation update)

Melanocyte protein Func 17 precursor (Melanocyte lineage-specific antigen GP100) (Melanoma-associated ME20 antigen) (ME20M/ME20S) (MM/ME20-S) (95 kDa melanocyte-specific secreted glycoprotein).

Mame=SILV; Synonyma=PMEL17, D12853E;

Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Harakawa T., Hara A., Hayatsu N., Hiranoto K., Hiraoka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Matsuyama T., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramara T., Yashiraki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai M., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-38-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
                                    SEQUENCE FROM N.A.
MEDLINE=92021023; PubMed=1924386;
                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6U; TISSUE=Whole body; MEDLINE=20530913; PubMed=11076861;
     Jenkins
                     Kwon B.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the E
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                                                                                                                                                                                                                                                                                                                                                                                            208
     N.A.,
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     Barton D.,
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Pred. No. 14;
                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                   C.A.,

    Copeland N.
    Kobayashi Y.,

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   .G., Gilbert D.J., Kim K.-K.;
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RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
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RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grinwood J., Schwutz J., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grinwood J., Sch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96154052; PubMed=8592076;
Bailin T., Lee S.-T., Spritz R.A.;
"Genomic organization and sequence
homologue of the mouse silver (si)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94327568; PubMed=7519602;
Adema G.J., de Boer A.J., Vogel A.M., Loenen W.A., Figdor C.G.;
"Molecular characterization of the melanocyte lineage-specific antigen gp100.";
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Hellstroem K.E., Marquardt H.;
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                 proteolytic cleavage.
TISSUE SPECIFICITY: Preferentially
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tissues nor in carcinomas. SIMILARITY: Belongs to the SIMILARITY: Contains 1 PKD

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EMBL; S73003; AAC60634.1; -.
EMBL; U31799; AAB00386.1; -.
EMBL; U31808; AAB00386.1; JOINED.
EMBL; U31807; AAB00386.1; JOINED.
EMBL; U3197; AAB00386.1; JOINED.
EMBL; U31798; AAB00386.1; JOINED.
EMBL; U01874; AAA10386.1; JOINED.
EMBL; U01874; AAA18479.1; -.
EMBL; U1491; AAB19181.1; JOINED.
EMBL; U1491; AAB19181.1; JOINED.
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Antigen; Direct protein s
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epeat; Signal; Transmembrane
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RA Klausner R.D., Collins F.S., Wagner L., Schammer C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,

RA Altopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.J., Lu X., Gibbs R.A.,

Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Xones S. Mayara M.A., Salska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S. T. Mayara M.A., Schmutz J., Schmerch A., Schein J.E.,

Jones S. T. Mayara M.A., Schmatha D.E., Schmerch A., Schein J.E.,

Jones S. T. Mayara M.A., Salska U., Smailus D.E., Schmerch A., Schein J.E.,
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Best Local :
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Q7ZVU9;
01-JUN-2003
01-JUN-2003
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AAP35866;
02-MAR-2004
02-MAR-2004
                      SEQUENCE FROM N. STRAIN=AB; TISSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
Nnpl protein (Fragment).
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Koundinya M., Raphael
Phelan M., Farmer A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAR-2004 (TrEMBLrel.
02-MAR-2004 (TrEMBLrel.
02-MAR-2004 (TrEMBLrel.
Silver homolog (Mouse).
                                                                                                                                      Jones S.J., Marra M.A.; "Generation and initial analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=AB; TISSUE=Whole body;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                     mouse
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8; Conserv
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                      TISSUE=Whole body
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AA; 70255 MW;
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full-length
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Catarrhini; Hominidae;
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RESULT 11
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ID AAS96
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DT 27-AE
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
HAMP domain protein.
OrderedLocusNames=DVUJ562;
                                     AAS96040;
27-APR-2004
27-APR-2004
11-MAY-2004
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DVU1562.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=15077118; DOI=10.1038/mbt959;
Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J., Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D., Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R., Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.; "The genome sequence of the anaerobic, sulfate-reducing bacterium Details of the state of the s
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                                                                                                                 AAS96040
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InterPro; IPR003660;
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PF01590; GAF; 1.
PF00672; HAMP; 1.
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                                                                                                                                                                                                                                                                                 Score 36; DB 2;
Pred. No. 1.1e+02;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB
Pred. No. 44;
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                                     annotation update)
                                                      sequence
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RESULT
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Best Local S
Matches 6
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01-OCT-2003
01-MAR-2004
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                                                                                                Gramene; Q7XUY6; -.
GO; GO:0008080; F:N-acetyltransferase
InterPro; IPR000182; GCN5acetyl_trans.
Pfam; PF00583; Acetyltransf 1; 1.
SEQUENCE 316 AA; 34542 MW; 36C799C
                                                                                                                                                                                                                  Lan L.,
Han B.;
                                                                                                                                                                                                                            Peng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
Weng Q., Zhang L., Lu Y., Lu Y., Zhang L.S., Yu Z., Fan D.,
Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                      "Sequence and analysis of rice Nature 420:316-320(2002). EMBL; AL606653; CAD40935.1; -.
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                                                                                                                                                                                                                                                                                                                                                               PubMed=12447439;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=OSJNBb0048E02.
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                                          Similarity 6; Conserv
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IMDQVPFSV
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(TrEMBLrel. 25,
(TrEMBLrel. 26,
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                                           Conservative
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                                                       77.8%;
66.7%;
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                                          Pred.
3; Mi
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Pred. No. 1.1e+02;
2; Mismatches 0
                                                                      Score
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                                                                                                   36C799C4C038EC66 CRC64;
                                                                                                                                                                                                      chromosome
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                                           Mismatches
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annotation
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                                                                                                                                             activity;
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a; Poales; Poaceae;
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RESULT Q9F6E7

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RESULT 14
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     Genome Res. 13:2577-2587(2003).

R EMBL; AP005338; BAC94966.1; -.

R GO; GO:0003677; F:DNA binding; IBA.

GO; GO:0008170; F:Ste-specific DNA-methyltransferase (ad

R GO; GO:0009170; F:site-specific DNA-methyltransferase (ad

R GO; GO:0006740; F:transferase activity; IEA.

R GO; GO:0016740; F:DNA methylation; IEA.

R GO; GO:0006306; P:DNA methylation; IEA.

R GO; GO:0006304; P:DNA modification; IEA.

R InterPro; IPR003665; Nethylase_M.

R InterPro; IPR003565; Nethylase.

InterPro; IPR003565; Nethylase.

InterPro; IPR003565; Nethylase.
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Q9F6E7;
01-MAR-2001
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Type I restriction-modification system methyltransferase subunit.
Name=VV2202;
                                                                                                                                                        PubMed=14656965;
Chen C.-Y., Wu K.-M., Chang Y.-C., Chang Liao T.-L., Liu Y.-M., Chen H.-J., Shen F. Shao C.-P., Lee C.-T., Hor L.-I., Tsai S. "Comparative genome analysis of Vibrio vu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Vibrionaceae; Vibrio. NCBI_TaxID=196600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000794; Ketoacyl_synth.
Pfam; PF00109; ketoacyl-synt; 1.
Pfam; PF02801; Ketoacyl-synt_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation updat
PKSA beta-ketoacylsynthase subunit beta.
                                                                                                                                               pathogen.";
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                                                                                                                                                                                                                                                                                    Vibrio vulnificus (strain
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66.7%;
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Gammaproteobacteria; Vibrionales;
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Search completed: December Job time : 13.9146 secs

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RESULT

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                                                                                                                                                                                    Transmembrane.
NON_TER 1
SEQUENCE 149
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Q94CH0;
01-DEC-2001
01-DEC-2001
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ
EMBL; AY029316; AAX38341.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0008219; P:cell death; IEA.
InterPro; IPR004326; Mlo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22456933; PubMed=12569425;
Devoco A., Hartmann H.A., Piffanelli P.,
Taramino G., Goh C.-S., Cohen P.E., Emers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4577;
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                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evol. 56:77-88(2003).
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  IMDHVPFIV
                                      IMDOVPESV
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(TrEMBLrel. 19, 1
3 (TrEMBLrel. 24, 1
3 membrane protein N
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2: uniprot_trembl:*
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01-MAY-2000 (TrEMBLrel. 13, 1
01-OCT-2003 (TrEMBLrel. 25, 1
CN 8 single chain antibody.
Name=CN 8 scPv;
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artificial sequences.
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CAG34081;
01-JUN-2004 (TrEMBLrel. 2
01-JUN-2004 (TrEMBLrel. 2
01-JUN-2004 (TrEMBLrel. 2
SCFV BBES protein (Fragme
SCFV BBES
                                                          SEQUENCE FROM N.A.
MEDLINE-20183931; PubMed-10706631;
Shinohara N., Demura T., Fukuda H.;
"Isolation of a vascular cell wall-specific monoclonal antibody recognizing a cell polarity by using a phage display subtraction method.";
                                                                                                                                                                                                                                                                                                                                                                              Q9QYF0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-DAID/C;
Peter J.C., Wallukat G., Tugler J., Mauric Briand J.P., Hoebeke J.;
"Modulation of the M2 muscarinic receptor "Modulation of the M2 muscarinic receptor";
                                                                                                                                                                                                         NCBI_TaxID=32630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-M2 receptor antibody fr
Submitted (JUN-2004) to the
EMBL; AJ746180; CAG34081.1;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                           Natl. Acad.
                       AB036341; BAA88633.1;
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Matches 141
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Best Local S
Matches 163
                                                                                                                                                                                                                                                                                                                                             MEDIINE=98170165; PubMed=9509426;
Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.I.
Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
"Cloning and characterization of cDNAs encoding VH monoclonal anti-CEA antibody (CEA 79) cross-reactive generation of a single-chain Fv molecule (scFv).";
Mol. Cells 7.816-819(1997).
EMBL; U88067; AAB48044.1; -.
PIR; S19965; S19965.
PIR; S19965; S19967.
PIR; S19967; S19967.
PIR; S19967; S26325.
PIR; S26325; S26325.
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HSSP, PO1820; LAYO.
InterPro; IPR0077110; Ig-like
InterPro; IPR0031506; Ig-v.
Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 2.
PROSITE; PSS0835; IG LIKE; 2
SEQUENCE 298 AA; 31867 MW
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01-DEC-2001 (TrEMBLrel. 19, L
01-MAR-2004 (TrEMBLrel. 26, L
Anti-CEA 79 single chain Fv (
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Q921A6;
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PROSITE;
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SMART; SM00406; IGv; 2.
PROSITE; PS50835; IG_LIKE;
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InterPro; IPR003596;
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                                                                                                        Similarity
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                                      QVKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIYDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL
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QVKLQQSGPELKKPGETVKISCKASGYTFTDYGMNWVKQAPGKGLKMMGWINTYTGEPTY
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241 AA;
                                                                                   55.9%; Score 710.5; DB 2; larity 58.3%; Pred. No. 1.4e-45; Conservative 34; Mismatches 56;
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Ig_v.
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68.5%; Pred. No. 4.6
Live 24; Mismatches
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Best Local S
Matches 135
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J. Biol. Chem. 278:36740-36747(2003).
EMBL; AJ574851; CAB00495-1;-
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; Ig; 2.
SMART; SM00406; IGv; 2.
PROSITE; PS50835; IG_LIKE; 2.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Peter J.C., Eftekhari P., Billiald P.,
"scFv single chain antibody variable f
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Name=scFv 6H8;
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01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                                                                                                                                                                      GGGSGGGGSGGGGSNIELTQSPAIMSASPGERVTMTCSASSSI-RYIYWYQQKPGSSPRL 179
                                                                                                                                                                                                                                                                                                                                  DEKFKNKGILTVDTSSSTAYMHLSSLASEDSAVYYCARG---GRGLDVWGAGTTLTVSSG
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[larity 56.5%;
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Pred. No. 3.2e-
38; Mismatches
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Sciurognathi; Muridae; Murinae;
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annotation update)
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No. 3.2e-44;
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Best Local
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EMBL; AF240168; ARX43733.1; -.

InterPro; IPRO07110; Ig-like.

InterPro; IPRO03596; Ig-v.

Pfam; PF00047; Ig; 1.

SMART; SM00406; IGv; 1.

PROSTTE; PS50835; IG LIKE; 1.

NON TER 218 218
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Q99KA4;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-MAR-2004 (TrEMBLrel. 2
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Mus musculus (Mouse).
Eukaryota; Metazoa; C
TIRSUE=Mammary tumor metastatized TISSUE=Mammary tumor metastatized MEDLINE=2388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Gr Klausner R.D., Collins F.S., Wagne
                                                                                                     LOC380791 protein.
Mus musculus (Mouse).
                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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STRAIN=BALB/c;
                                                     SEQUENCE
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Rodentia;
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Rodentia;
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Pred. No. 2e-36;
6; Mismatches
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Matches 127; Conserv
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     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                  Pterin-mimicking
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PROSITE; PS00290; IG_MHC; UNKNOWN_2.

SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;
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                                  musculus (Mouse)
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R.F., Jordan
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation updat
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Pred. No. 1.1e
16; Mismatches
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36;
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                                                                                      TISSUE-Manmary tumor metastatized to lung. MMTV-LTR/Wnt1 model.

RC Expression driven by an MMTV-LTR enhancer.;

RX MEDLINE=23388257; PubMed=12477932;

RX MEDLINE=23388257; PubMed=12477932;

RX MEDLINE=23388257; PubMed=12477932;

RX MISSUE R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RX Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Moclean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S. J. Marra M.A.;

RA Jones S. J. Marra M.A.;
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Best Local S
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Q91Z07;
Q1-DEC-2001
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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PIR; C25913; C25913.
HSSP; P01783; 1IGC.
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NON_TER 1 1 1
NON_TER 119 119
SEQUENCE 119 AA; 13025 N
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                                                  Jones S.J., Marra M.A.; "Generation and initial analysis
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InterPro; IPR003596;
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                            mouse cDNA sequences.";
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Rodentia;
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to the EMBL/GenBank/DDBJ
     U.S.A.
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Pred. No. 2
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     99:16899-16903 (2002)
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Expression driven by an Male Strausberg R.;

Submitted (JUL-2001) to the EMBL/
R MSSP; P01789; IMCP.

InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003596; Ig MHC.
InterPro; IPR003596; Ig WHC.
InterPro; IPR003596; Ig V.
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EDUENCE FROM N.A.

C STRAIN-FVB/N; TISSUE-COlon;

C MEDLING-22388257; PubMed=12477932;

C MEDLING-2388257; PubMed=12477932;

C MEDLING-2388257; PubMed=12477932;

C A Strausberg R.L., Feingold E.A., Grouse L.H., Schaefer C.P., Bhat N.K.,

C A Altechul S.F., Zeeberg B., Duetow K.H., Schaefer C.P., Bhat N.K.,

C A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

C A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

C A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Scheetz T.E.,

C A Hopkins R.F., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

C A Brownstein M.J., Goares M.B., Bonaldo M.F., Carninci P., Prange C.,

C A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

C A Raha S.S., MocEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

C A Raha S.S., MocEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

C A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

C A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

C A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

C A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

C A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

C A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

C A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

C A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

C A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

C A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

C A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

C A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

C A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

C A Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L
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Best Local S
Matches 117
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SEQUENCE FROM
STRAIN=Czech
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Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
SMOSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN
SEQUENCE 486 AA; 52681 MW; 4FE
                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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Name=Igh-VJ558;
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117; Conserv
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Pred. No. 1
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Sciurognathi; Muridae;
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                     C. Y S.J.
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Best Local S
Matches 115
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InterPro; IPR003357; Ig_cl.
InterPro; IPR003357; Ig_wHC.
InterPro; IPR003596; Ig_v.
Ffam; PP07654; Cl-set; Z.
Pfam; PP0047; Ig; 1.
SMART; SM00406; IGv; 1.
MEDLINE=2388257; PubMed=12477932;

MEDLINE=2388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci R.D., Mullahy S.J.,
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PROSITE; 1
NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-2001) to the EMBL; BC010798; AAH10798.1; HSSP; P01789; 1MCP.
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"Generation and initial analysis
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Natl. Acad. Sci. U.S.
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Primates;
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Pred. No. 3.9e-29;
0; Mismatches 46
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G.G.,
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RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUB=Colon;

RX MEDLINE=22388257; PubMed=12477932;

RX MEDLINE=22388257; PubMed=12477932;

RX Altausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altausher R.D., Collins F.S., Wagner L., Shenmen C.M., Haish F.,

RA Altausher R.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,

RA Altausher R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

RA Altausher R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Gay L.J., Hulyk S.W.,

RA Hitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Standard J., Myers R.M., Butterfield Y. Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.
                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2002) to the EMBL; BC024289; AAH24289.1; Hypothetical protein. SEQUENCE 471 AA; 51791 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q91WP5
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                                                                                                                                                                                                                                                                                                                                                                                                                            Igh-VJ558 protein
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c. Natl. Acad. Sci. U.S
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Pred. No. 1.8e-28
3; Mismatches 6
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Sciurognathi; Muridae;
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Gibbs R.A.,
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; Murinae; Mus
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A., Schein J.E.,
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Matches 113
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HSSP; P01789; IMCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig c1.
InterPro; IPR003597; Ig_MHC.
InterPro; IPR003906; Ig_MHC.
InterPro; IPR00396; Ig_v.
Pfam; PF007654; C1-set; 2.
Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
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AAR11048;
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02-MAR-2004
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SEQUENCE
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"Generation and initial analysis
and mouse cDNA sequences.":
                                                                                                                                                                                                                             STRAIN-B6.Sle1; TISSUE-Splee
Liang Z., Xie C., Chen C., K
"Antinuclear autoantibodies
Submitted (SEP-2003) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNP
SEQUENCE 479 AA; 51603 MW;
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation updat
02-MAR-2004 (TrEMBLrel. 27, Last annotation updat
ANA immunoglobulin kappa light chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
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                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krzywinski M.I., Skalska U.,
138 LTQSPAIMSASPGERVTMTCSASSSIRYIYWYQQKPGSSPRLLIYDTSNVAPGVPPRFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113;
                                                                                                                                                                                                            AY436888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
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                                                            l Similarity
87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARGNWEGWYFDVWGQGTTVTVSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTFDKRLEWVATISSGGSYTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCLIHDYFPSGTMNVTWGKSGKDITTVNFFPALASGGRYTMSSQLTLPAVECPEGESVKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGSGGGGGGGSNIELTQSPAIMSASPGERVTMTCSASSSIRYIYWYQQKPGSSPRL-
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                                                                Conservative
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                                                                                                                                                ΑA;
                                                                                                                                                                                                                                                                      TISSUE=Spleen;
, Chen C., Kre
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                                                                                                                                                                     108
                                                                                                                                                                                                                                                                                                                                                                             Rodentia;
                                                                                 37.6%;
87.0%;
                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
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47.1%;
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                                                                                                                                                ΜW.;
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MW; ECB2D0877748584F
                                                                                                                                                                                                                                                  Kreska D., Hsu
s from B6.Sle1 r
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                                                                                                                                                                                                                               from B6.Sle1 mice
EMBL/GenBank/DDBJ
                                                              9;
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Pred. No. 1.8e
L9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ
                                                                                                     Score 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smailus
                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; 1
Sciurognathi; Muridae;
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                                                                                                                                             C11222F2FDFBC160
                                                              Mismatches
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                                                              Indels
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ID QGGMY2
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X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Klausner R.D., Collins F.S., Wagner A.A., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang L.,

X Buchwastein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

X Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

X Brownstein M.J., Wallano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X Bosak S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

X Villalon B., Ketteman M., Madan A., Gotrigues S., Sanchez A.,

X Pahey J., Helton B., Ketteman M., Madan A., Bouffard G.G.,

X Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

X Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

X Hones S. J. Marra M.A.,

X Jones S. J. Marra M.A.,

X Jones S. J. Marra M.A.
                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 95
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InterPro; IPR003597; Ig.-1ke.
InterPro; IPR003597; Ig.-1ke.
InterPro; IPR003597; Ig.-2k.
InterPro; IPR003596; Ig.-yk.
InterPro; IPR003596; Ig.-yk.
InterPro; IPR00396; Ig.-yk.
InterPro; IPR00396; Ig.-yk.
InterPro; IPR00396; Ig.-yk.
InterPro; IPR00306; Ig.-yk.
InterPro; IRV00409; IG.-yk.
INTERPOSITE; INTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-2004) to the EMBL; BC073758; AAH73758.1;
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.
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                                                                                                                          QVKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYY
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                                                                             QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSSSYTNY
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                                                                                                                                                                                                                                                                                                                                                                                                   66184 MW; B6B38B51114E4C55 CRC64;
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                                                                                                                                                                                                                                                                        Score 477.5; DB 2;
Pred. No. 1.2e-27;
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Best Local S
Matches 98
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Hypothetical protein.

SEQUENCE 464 AA; 51099 MM; 2FCA7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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05-JUL-2004 (TrEMBLrel. 27,
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TISSUE=Human rectum tumor;
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Name=DKFZp686C15213;
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  ne : 189.085
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                                                                                                                                                      SGGGGSGGGGGGSNIELTQSPAIMSASPGERVTMTCSASSS
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Pred. No. 1.4e-27;
8; Mismatches 20
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